wwPDB X-ray Structure Validation Summary Report (i)

Aug 23, 2023 – 04:19 AM EDT

PDB ID	:	3BLX
Title	:	Yeast Isocitrate Dehydrogenase (Apo Form)
Authors	:	Taylor, A.B.; Hu, G.; Hart, P.J.; McAlister-Henn, L.
Deposited on	:	2007-12-11
Resolution	:	2.70 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

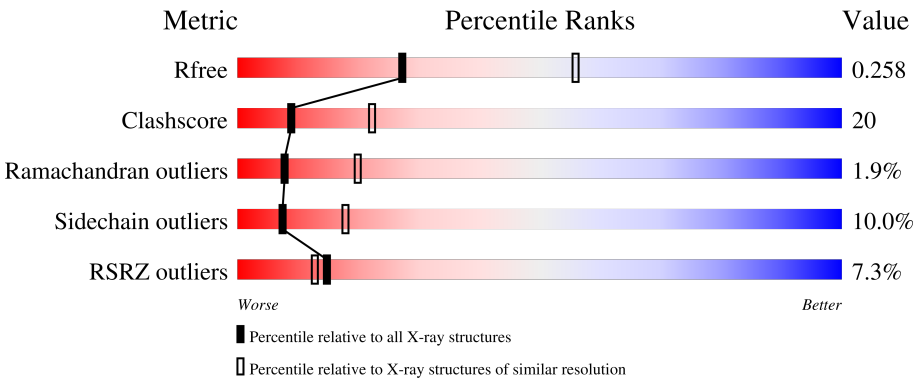
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	349	4% 65% 27%
1	C	349	% 66% 27%
1	E	349	% 68% 25%
1	G	349	% 65% 26%
1	I	349	4% 64% 26% 5% 5%

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Mol	Chain	Length	Quality of chain
1	K	349	66% 26% 5%
1	M	349	19% 62% 30% 5%
1	O	349	% 67% 25% 5%
2	B	354	4% 62% 30% 6%
2	D	354	5% 55% 36% 6%
2	F	354	11% 56% 36% 6%
2	H	354	10% 55% 36% 6%
2	J	354	6% 58% 34% 6%
2	L	354	10% 57% 34% 6%
2	N	354	19% 55% 35% 8%
2	P	354	15% 55% 31% 6% 8%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 41336 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Isocitrate dehydrogenase [NAD] subunit 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	335	2575	1626	451	491	7	0	0	0
1	C	338	2605	1645	458	495	7	0	0	0
1	E	341	2626	1659	461	499	7	0	0	0
1	G	334	2567	1620	450	490	7	0	0	0
1	I	333	2562	1617	448	490	7	0	0	0
1	K	338	2605	1645	458	495	7	0	0	0
1	M	337	2590	1638	453	492	7	0	0	0
1	O	332	2546	1605	447	487	7	0	0	0

- Molecule 2 is a protein called Isocitrate dehydrogenase [NAD] subunit 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	346	2608	1646	447	509	6	0	0	0
2	D	345	2598	1640	444	508	6	0	0	0
2	F	345	2598	1640	444	508	6	0	0	0
2	H	345	2598	1640	444	508	6	0	0	0
2	J	345	2598	1640	444	508	6	0	0	0
2	L	346	2608	1646	447	509	6	0	0	0

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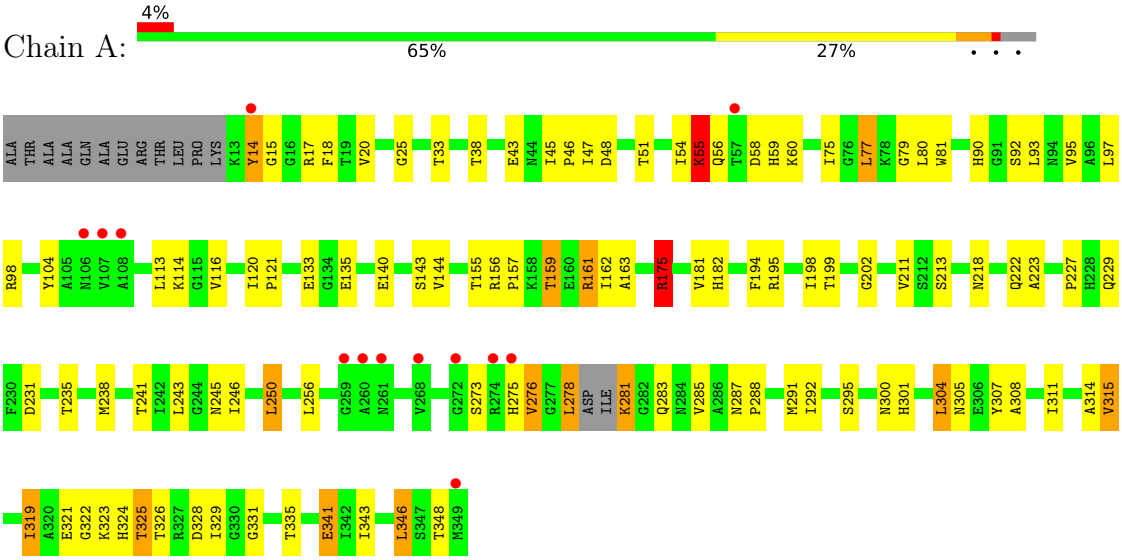
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	N	345	2598	1640	444	508	6	0	0	0
			Total	C	N	O	S			
2	P	326	2454	1549	418	481	6	0	0	0

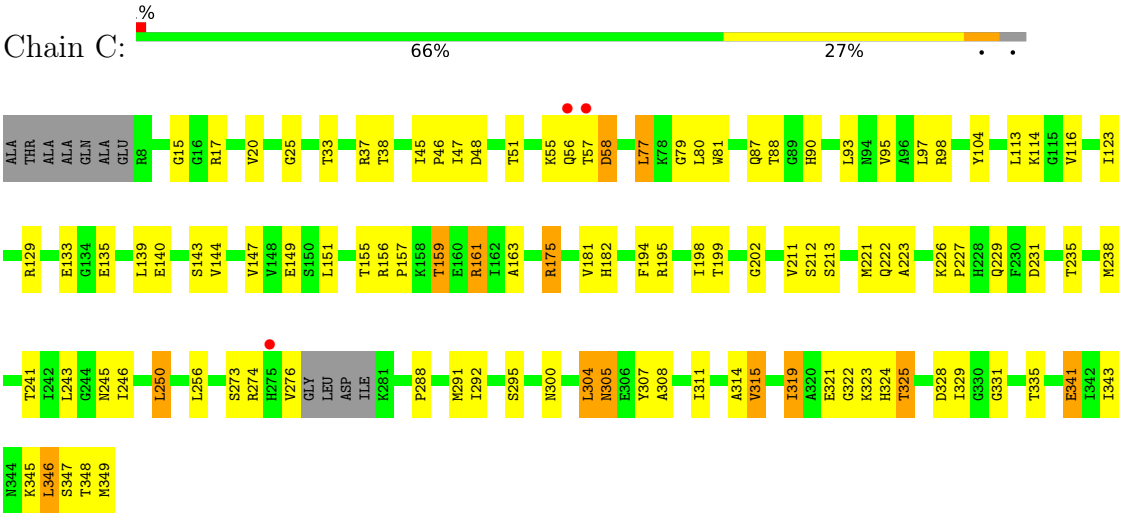
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

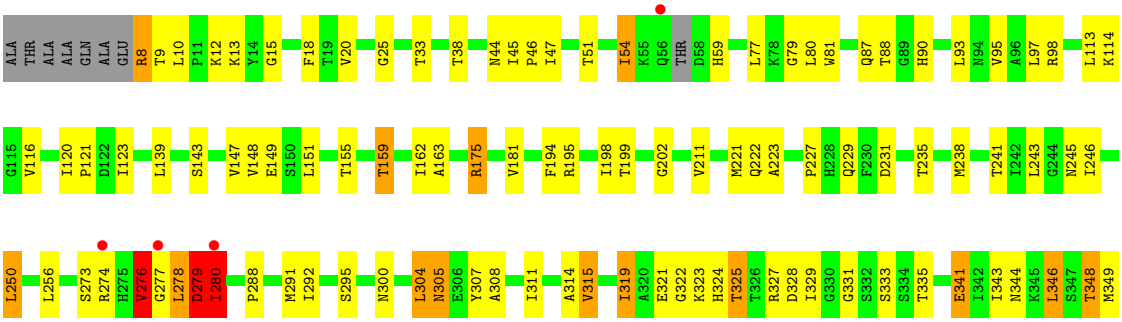
• Molecule 1: Isocitrate dehydrogenase [NAD] subunit 1



• Molecule 1: Isocitrate dehydrogenase [NAD] subunit 1

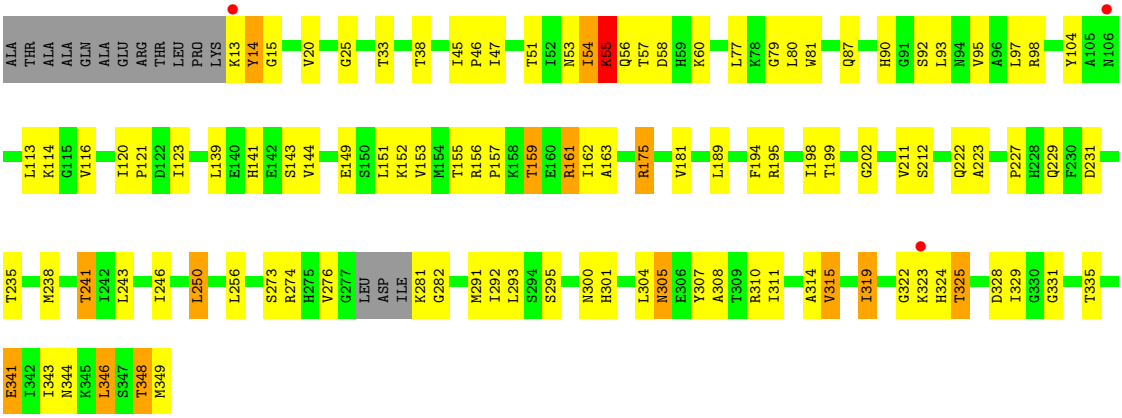


• Molecule 1: Isocitrate dehydrogenase [NAD] subunit 1



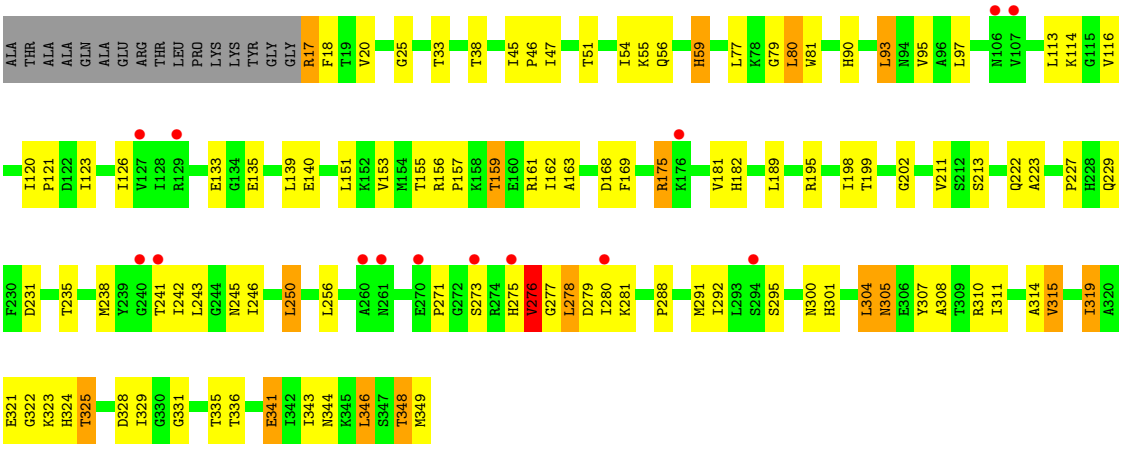
• Molecule 1: Isocitrate dehydrogenase [NAD] subunit 1

Chain G:



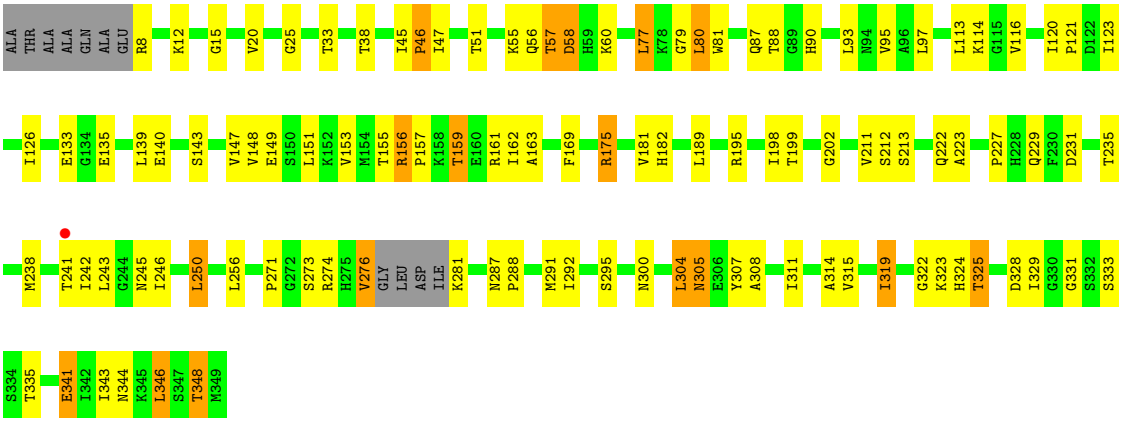
• Molecule 1: Isocitrate dehydrogenase [NAD] subunit 1

Chain I:



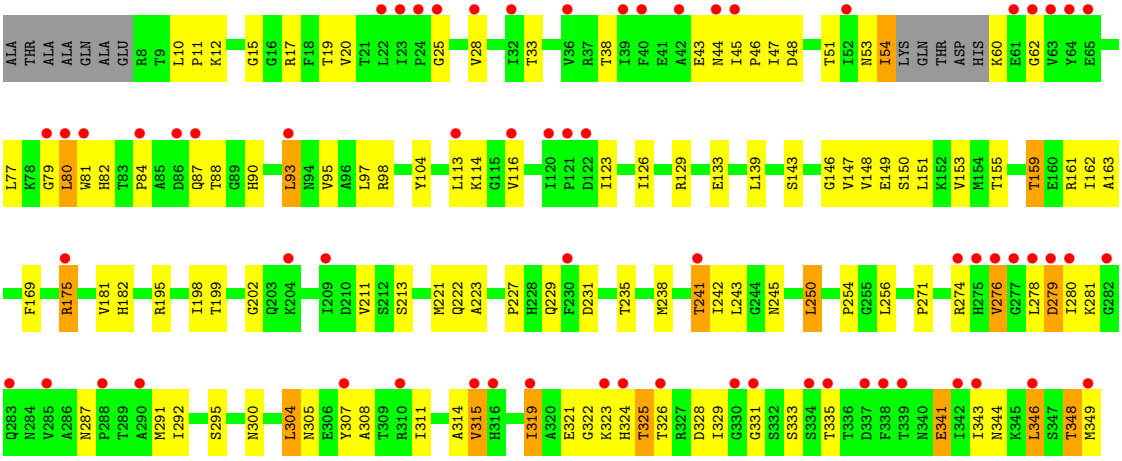
• Molecule 1: Isocitrate dehydrogenase [NAD] subunit 1

Chain K:



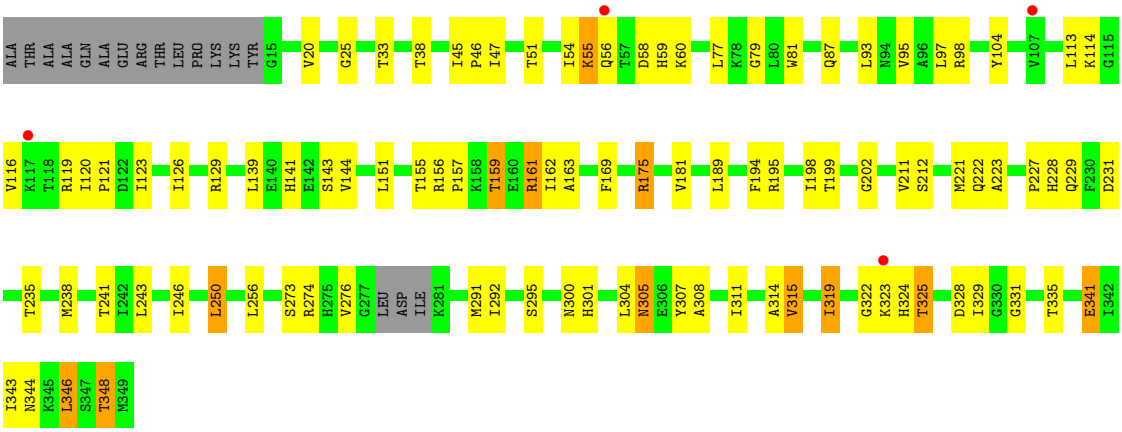
• Molecule 1: Isocitrate dehydrogenase [NAD] subunit 1

Chain M:



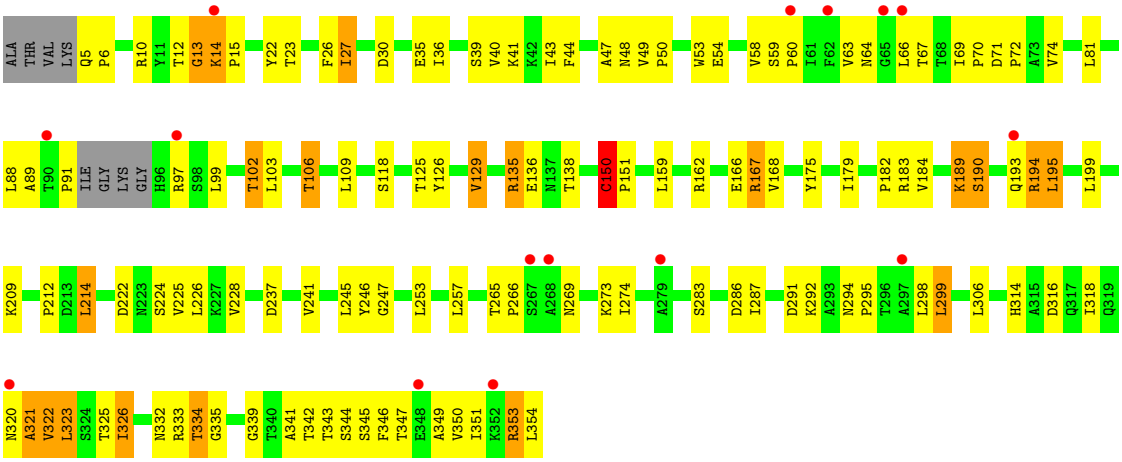
• Molecule 1: Isocitrate dehydrogenase [NAD] subunit 1

Chain O:



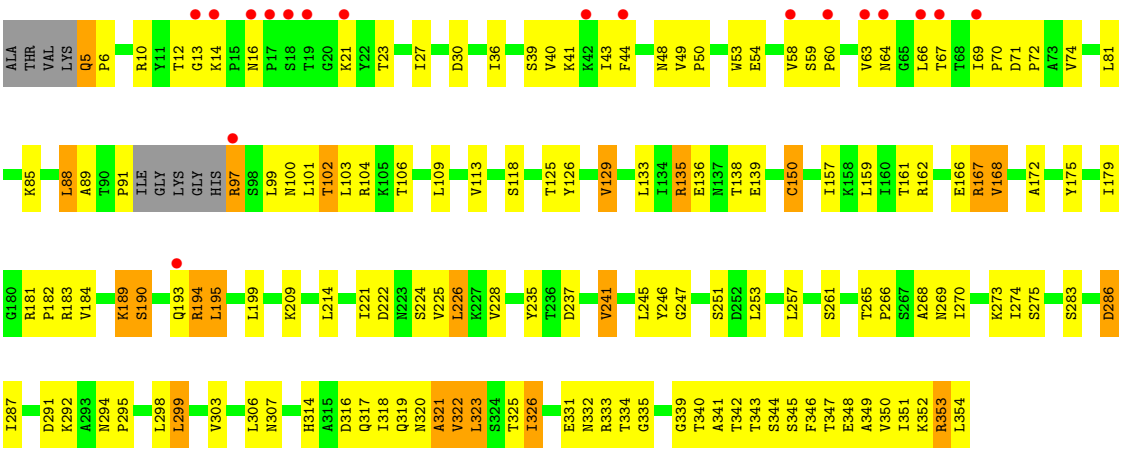
• Molecule 2: Isocitrate dehydrogenase [NAD] subunit 2

Chain B:



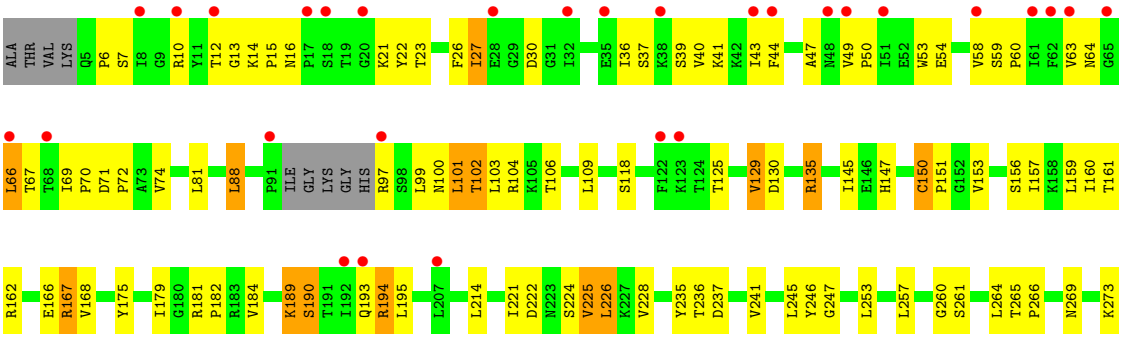
- Molecule 2: Isocitrate dehydrogenase [NAD] subunit 2

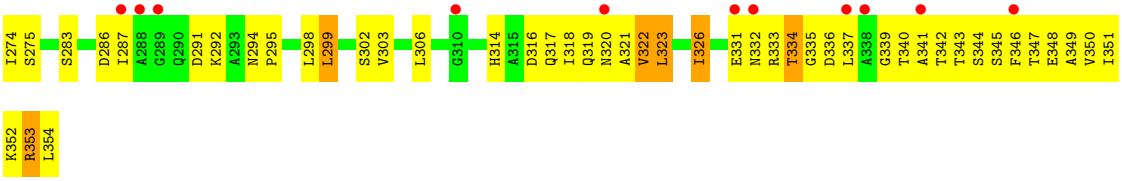
Chain D:



- Molecule 2: Isocitrate dehydrogenase [NAD] subunit 2

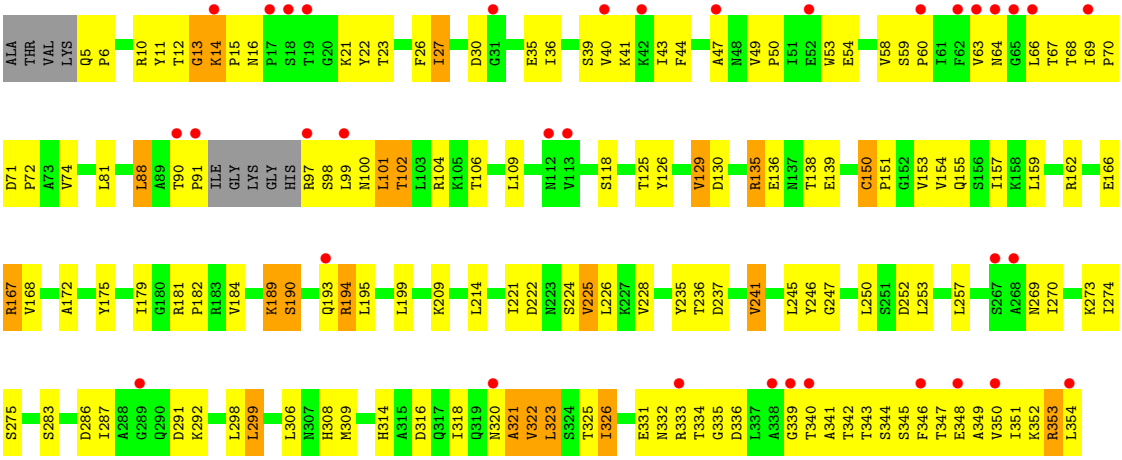
Chain F:





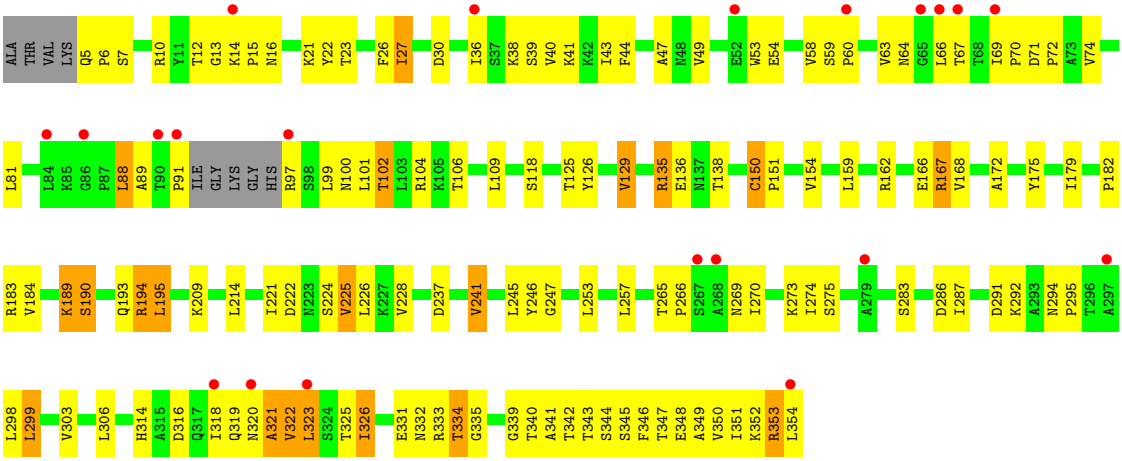
• Molecule 2: Isocitrate dehydrogenase [NAD] subunit 2

Chain H:



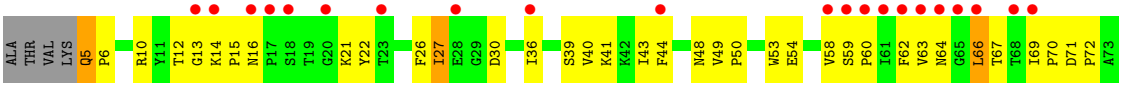
• Molecule 2: Isocitrate dehydrogenase [NAD] subunit 2

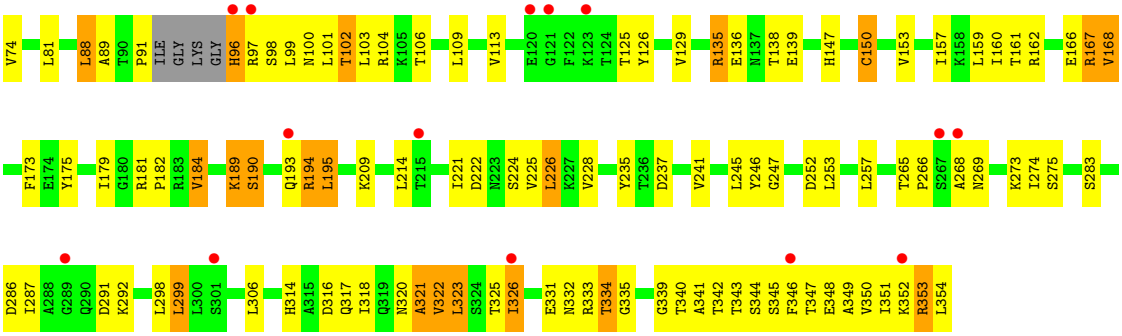
Chain J:



• Molecule 2: Isocitrate dehydrogenase [NAD] subunit 2

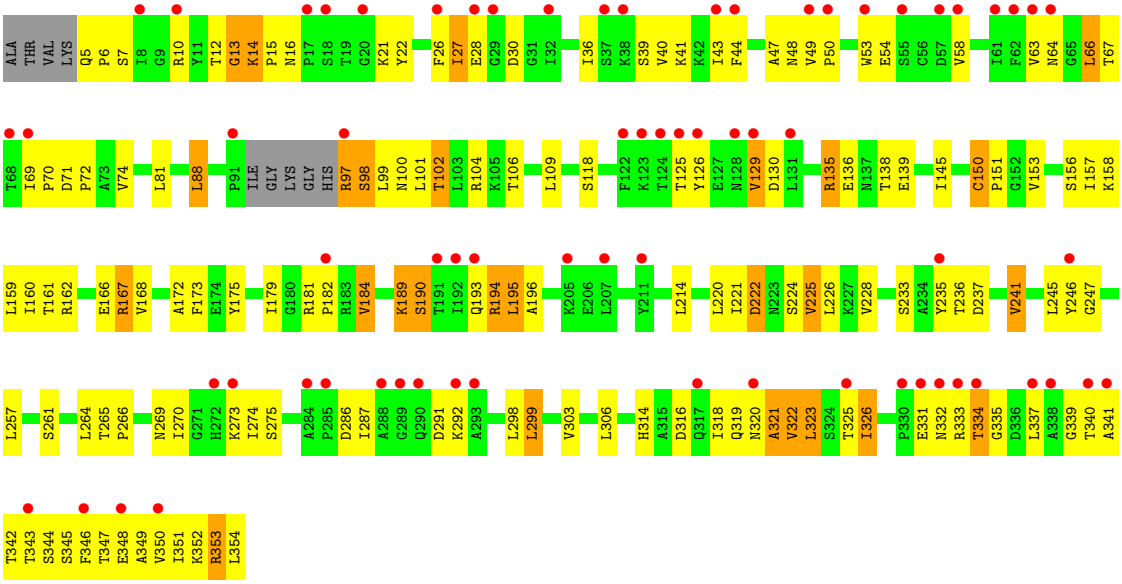
Chain L:





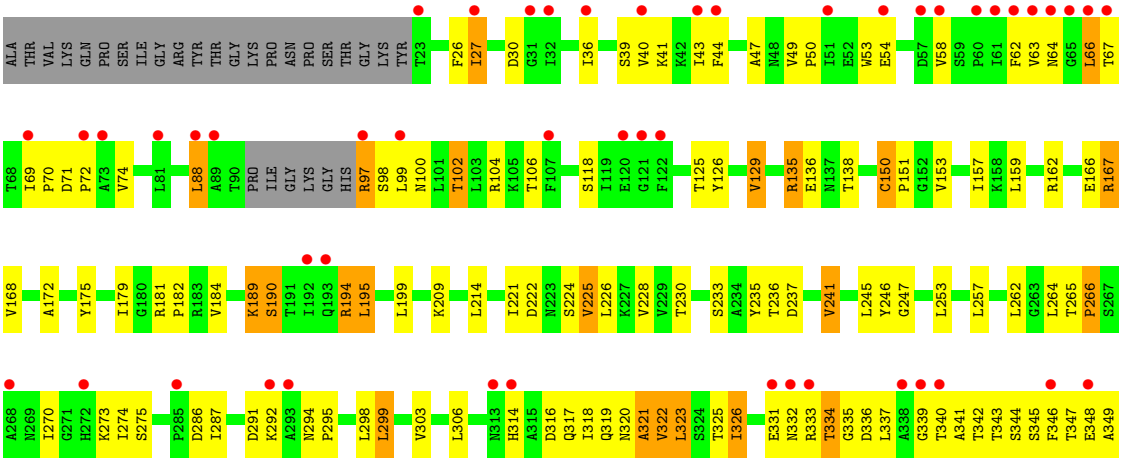
- Molecule 2: Isocitrate dehydrogenase [NAD] subunit 2

Chain N:



- Molecule 2: Isocitrate dehydrogenase [NAD] subunit 2

Chain P:



V350
I351
K352
R353
L354

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	112.44Å 115.21Å 159.25Å 111.03° 96.08° 107.13°	Depositor
Resolution (Å)	35.74 – 2.70 35.74 – 2.70	Depositor EDS
% Data completeness (in resolution range)	96.5 (35.74-2.70) 96.5 (35.74-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$< I/\sigma(I) >$ [1]	2.01 (at 2.68Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, R_{free}	0.239 , 0.264 0.231 , 0.258	Depositor DCC
R_{free} test set	9220 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å^2)	71.3	Xtriage
Anisotropy	0.225	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 43.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.005 for k,h,-h-k-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	41336	wwPDB-VP
Average B, all atoms (Å^2)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.80% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A	0.60	0/2619	0.71	2/3538 (0.1%)
1	C	0.60	0/2650	0.67	0/3580
1	E	0.56	0/2671	0.69	0/3608
1	G	0.56	0/2611	0.67	0/3527
1	I	0.58	0/2606	0.68	0/3524
1	K	0.57	0/2650	0.67	0/3580
1	M	0.64	0/2634	0.69	0/3559
1	O	0.54	0/2589	0.66	0/3498
2	B	0.51	1/2654 (0.0%)	0.62	0/3610
2	D	0.48	0/2643	0.62	1/3595 (0.0%)
2	F	0.47	0/2643	0.60	0/3595
2	H	0.46	0/2643	0.59	0/3595
2	J	0.43	0/2643	0.56	0/3595
2	L	0.46	1/2654 (0.0%)	0.60	0/3610
2	N	0.50	0/2643	0.59	0/3595
2	P	0.46	0/2493	0.59	0/3390
All	All	0.53	2/42046 (0.0%)	0.64	3/56999 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	M	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L	150	CYS	CB-SG	5.76	1.92	1.82
2	B	150	CYS	CB-SG	5.60	1.91	1.82

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	175	ARG	NE-CZ-NH1	5.99	123.30	120.30
2	D	150	CYS	CA-CB-SG	5.47	123.84	114.00
1	A	278	LEU	CA-CB-CG	5.40	127.72	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	M	53	ASN	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2575	0	2608	87	0
1	C	2605	0	2645	85	0
1	E	2626	0	2667	94	0
1	G	2567	0	2597	89	0
1	I	2562	0	2596	90	0
1	K	2605	0	2645	82	0
1	M	2590	0	2635	116	0
1	O	2546	0	2575	82	0
2	B	2608	0	2648	124	0
2	D	2598	0	2641	138	0
2	F	2598	0	2641	151	0
2	H	2598	0	2641	148	0
2	J	2598	0	2641	132	0
2	L	2608	0	2648	138	0
2	N	2598	0	2641	169	0
2	P	2454	0	2498	124	0
All	All	41336	0	41967	1692	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 20.

The worst 5 of 1692 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:97:ARG:NH1	2:N:102:THR:HG23	1.63	1.12
1:E:54:ILE:H	1:E:54:ILE:HD12	1.19	1.06
1:O:181:VAL:HB	1:O:235:THR:HG22	1.37	1.04
1:E:181:VAL:HB	1:E:235:THR:HG22	1.38	1.04
1:A:181:VAL:HB	1:A:235:THR:HG22	1.38	1.03

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	331/349 (95%)	311 (94%)	16 (5%)	4 (1%)	13	32
1	C	334/349 (96%)	315 (94%)	16 (5%)	3 (1%)	17	40
1	E	337/349 (97%)	320 (95%)	12 (4%)	5 (2%)	10	26
1	G	330/349 (95%)	309 (94%)	14 (4%)	7 (2%)	7	18
1	I	331/349 (95%)	310 (94%)	16 (5%)	5 (2%)	10	26
1	K	334/349 (96%)	315 (94%)	15 (4%)	4 (1%)	13	32
1	M	333/349 (95%)	315 (95%)	15 (4%)	3 (1%)	17	40
1	O	328/349 (94%)	309 (94%)	16 (5%)	3 (1%)	17	40
2	B	342/354 (97%)	310 (91%)	23 (7%)	9 (3%)	5	13
2	D	341/354 (96%)	307 (90%)	25 (7%)	9 (3%)	5	13
2	F	341/354 (96%)	307 (90%)	26 (8%)	8 (2%)	6	16
2	H	341/354 (96%)	304 (89%)	29 (8%)	8 (2%)	6	16
2	J	341/354 (96%)	309 (91%)	24 (7%)	8 (2%)	6	16
2	L	342/354 (97%)	306 (90%)	27 (8%)	9 (3%)	5	13
2	N	341/354 (96%)	301 (88%)	30 (9%)	10 (3%)	4	10
2	P	322/354 (91%)	289 (90%)	27 (8%)	6 (2%)	8	20

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	5369/5624 (96%)	4937 (92%)	331 (6%)	101 (2%)	8 20

5 of 101 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	304	LEU
1	C	58	ASP
1	C	304	LEU
1	E	276	VAL
1	E	304	LEU

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	279/289 (96%)	252 (90%)	27 (10%)	8 19
1	C	283/289 (98%)	254 (90%)	29 (10%)	7 17
1	E	285/289 (99%)	250 (88%)	35 (12%)	4 11
1	G	278/289 (96%)	248 (89%)	30 (11%)	6 15
1	I	279/289 (96%)	251 (90%)	28 (10%)	7 18
1	K	283/289 (98%)	252 (89%)	31 (11%)	6 14
1	M	281/289 (97%)	254 (90%)	27 (10%)	8 19
1	O	276/289 (96%)	249 (90%)	27 (10%)	8 18
2	B	292/297 (98%)	264 (90%)	28 (10%)	8 19
2	D	291/297 (98%)	263 (90%)	28 (10%)	8 19
2	F	291/297 (98%)	262 (90%)	29 (10%)	7 18
2	H	291/297 (98%)	263 (90%)	28 (10%)	8 19
2	J	291/297 (98%)	263 (90%)	28 (10%)	8 19
2	L	292/297 (98%)	263 (90%)	29 (10%)	8 18
2	N	291/297 (98%)	265 (91%)	26 (9%)	9 22
2	P	275/297 (93%)	248 (90%)	27 (10%)	8 18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	4558/4688 (97%)	4101 (90%)	457 (10%)	7 18

5 of 457 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	323	LEU
2	P	195	LEU
2	J	323	LEU
2	P	150	CYS
2	N	323	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	O	283	GLN
2	P	155	GLN
1	I	90	HIS
1	I	301	HIS
2	J	155	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	335/349 (95%)	-0.04	13 (3%)	39	38	13, 38, 80, 100	0
1	C	338/349 (96%)	-0.08	3 (0%)	84	85	11, 38, 75, 93	0
1	E	341/349 (97%)	-0.15	4 (1%)	79	80	18, 42, 78, 117	0
1	G	334/349 (95%)	-0.08	3 (0%)	84	85	16, 41, 79, 96	0
1	I	333/349 (95%)	0.05	14 (4%)	36	35	17, 40, 78, 113	0
1	K	338/349 (96%)	-0.17	1 (0%)	94	95	13, 41, 78, 98	0
1	M	337/349 (96%)	0.90	66 (19%)	1	0	21, 48, 91, 121	0
1	O	332/349 (95%)	-0.20	4 (1%)	79	80	17, 43, 79, 97	0
2	B	346/354 (97%)	0.27	15 (4%)	35	33	21, 60, 102, 119	0
2	D	345/354 (97%)	0.22	18 (5%)	27	25	21, 66, 105, 123	0
2	F	345/354 (97%)	0.51	40 (11%)	4	3	24, 69, 107, 121	0
2	H	345/354 (97%)	0.47	35 (10%)	7	5	24, 69, 108, 127	0
2	J	345/354 (97%)	0.46	21 (6%)	21	20	24, 67, 105, 120	0
2	L	346/354 (97%)	0.42	35 (10%)	7	5	24, 69, 106, 121	0
2	N	345/354 (97%)	1.05	69 (20%)	1	0	28, 77, 111, 122	0
2	P	326/354 (92%)	0.72	54 (16%)	1	1	30, 74, 109, 119	0
All	All	5431/5624 (96%)	0.27	395 (7%)	15	13	11, 53, 103, 127	0

The worst 5 of 395 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	N	341	ALA	9.6
2	N	192	ILE	7.9
2	P	65	GLY	7.0
1	M	62	GLY	6.9
1	M	275	HIS	6.7

6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.